Highly parallel genome-wide expression analysis of single mammalian cells.

Journal: PLoS One

Publication Year: 2012

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PubMed link: 22347404

Funding Grants: Ensuring the safety of cell therapy: a quality control pipeline for cell purification and validation

Public Summary:
BACKGROUND: We have developed a high-throughput amplification method for generating robust gene expression profiles using single cell or low RNA inputs. METHODOLOGY/PRINCIPAL FINDINGS: The method uses tagged priming and template-switching, resulting in the incorporation of universal PCR priming sites at both ends of the synthesized cDNA for global PCR amplification. Coupled with a whole-genome gene expression microarray platform, we routinely obtain expression correlation values of R(2)~0.76-0.80 between individual cells and R(2)~0.69 between 50 pg total RNA replicates. Expression profiles generated from single cells or 50 pg total RNA correlate well with that generated with higher input (1 ng total RNA) (R(2)~0.80). Also, the assay is sufficiently sensitive to detect, in a single cell, approximately 63% of the number of genes detected with 1 ng input, with approximately 97% of the genes detected in the single-cell input also detected in the higher input. CONCLUSIONS/SIGNIFICANCE: In summary, our method facilitates whole-genome gene expression profiling in contexts where starting material is extremely limiting, particularly in areas such as the study of progenitor cells in early development and tumor stem cell biology.

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